SYNOPSIS OF RESEARCH PROJECT

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4.	**Name of the Degree Submitted for**	**:**	Ph. D.
5.	**Major Subject**	**:**	Genetics and Plant Breeding
6.	**Minor Subject**	**:**	Molecular Biology and Biotechnology
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8.	**Title of Research Project**	**:**	**GENETIC ANALYSIS FOR GRAIN YIELD AND ITS CONTRIBUTING TRAITS IN SINGLE *v/s* THREE-WAY CROSS IN MAIZE (*Zea mays* L.)**

9. Introduction

Maize (*Zea mays* L.), often referred as corn, is one of the most prominent cereal grains broken-down worldwide in tropical, subtropical and humid environments. Maize originated from a wild grass called *Teosinte*, which was native to Central America and due to millennia of selective breeding and domestication has come to be one of the most diverse and adaptable crop species known. This crop shows exceptional phenotypic plasticity and genetic variation, allowing it to be adapted to diverse agro-ecological environments from the lowland tropics to cool temperate highland situations (Hallauer *et al*., 2010). Maize is popularly called as “Queen of cereals” because of its wide adaptability.

In terms of overall output and productivity, maize is the most productive cereal crop in the world, outperforming wheat and rice. More than 160 nations cultivate it, with the US, China, Brazil and India being the top producers. Maize is essential for

industrial uses, animal feed and global food security. The grain's nutritional and physiological advantages are attributed to its high content of proteins, carbs, vitamins and minerals as well as bioactive substances such phenolics and carotenoids (Shiferaw *et al*., 2011).

After rice and wheat, In terms of economic significance, corn is the third most significant grain crop in India. India is the world's largest producer of maize, with 43.40 million tonnes produced from 12 million hectares of land and a productivity of 3,590.10 kg/hectare in 2024–2025. Madhya Pradesh and Karnataka are the Indian states with the largest areas planted to maize (2.30 million hectares and 1.91 million hectares, respectively), followed by Rajasthan (1.01 million hectares) and Maharashtra (1.63 million hectares). The states that produce the most maize are Madhya Pradesh (6.64 million tonnes), Karnataka (6.19 million tonnes) and Bihar (5.47 million tonnes). The most productive state is West Bengal (6,998.90 kg/ha), followed by Andhra Pradesh (6,510.40 kg/ha) and Bihar (6,100.50 kg/ha). Gujarat, on the other hand, produces 0.79 million tonnes of grain with a mean productivity of 1,858.3 kg/ha from its 0.42 million hectares of land (Anonymous, 2025). The crop is mostly cultivated under rainfed circumstances throughout the *kharif* season, while irrigation and better hybrid cultivars are boosting its cultivation during the winter and spring seasons.

There is a minimal amount of maize produced by a number of factors, despite its significance and growing demand. Numerous genes control the complicated quantitative characteristic of grain yield, which is heavily impacted by environmental variables. Finding stable and high-yielding genotypes in various contexts is sometimes made more difficult by the existence of considerable Genotype × Environment Interaction (GEI) (Gauch, 2013). Crop production and stability are also negatively impacted by a number of biotic stressors, including stem borers, fall armyworm (*Spodoptera frugiperda*) and diseases including *Turcicum* leaf blight and downy mildew.

The most effective method for increasing maize output has been hybrid breeding. The genetic makeup, degree of heterosis and adaptability of various hybrid kinds, such as single cross, double cross and three-way cross hybrids, vary. While double cross and three-way hybrids frequently demonstrate superior buffering capacity and stability under varying environmental circumstances, single cross hybrids typically display higher production potential and uniformity (Hallauer and Miranda, 1988). Therefore,

assessing these hybrids in a variety of settings is crucial to comprehending their stability and performance.

10. Practical Utility of the Research Project

The current study offers useful data for bolstering programmes aimed at improving maize. Finding hybrids with reliable and excellent performance is made easier by evaluating the kind and extent of heterosis for grain yield and its constituent characteristics in various settings. These heterotic combinations are directly helpful in creating commercial hybrids that can sustain high production in the face of shifting climate circumstances.

For plant breeders who want to create better varieties and increase production potential, finding appropriate parental lines is essential. It is not always the case that a genotype with high yield would successfully pass on its desired features to its offspring. Therefore, a major component of successful breeding programs is the availability of advantageous gene combinations, especially in the form of strong combining inbred lines. Selecting suitable parents and prospective cross combinations requires an understanding of combining ability, which is crucial for creating better hybrids. It also sheds light on the genetic processes that control how different features are inherited. Therefore, in plant breeding projects, combining ability analysis is a useful method for separating successful combiners from less effective ones.

For more than 50 years, plant breeders have effectively estimated the relative combining ability of lines using the diallel mating design. Plant breeders can estimate differences in general combining ability (GCA) and specialised combining ability (SCA) from the diallel mating design. GCA is “the average performance of a line in hybrid combinations,” whereas SCA is “those cases in which certain combinations do relatively better or worse than would be expected on the basis of the average performance of the lines involved”, according to Sprague and Tatum (1942). In order to improve the effectiveness of maize breeding programmes, the diallel analysis approach has been widely utilised for parental selection as a suitable scheme to quickly gather genetic information about grain yield and its component qualities. Combining ability analysis, which was created by Griffing in 1956, is seen to be more beneficial to maize breeders among the many diallel approaches. It offers important information on parents capacity to pass on favourable features to their offspring (Seboka and Singh, 2009). The ability to offer a comprehensive genetic picture of experimental material in a single generation is another benefit of diallel analysis.

Deeper understanding of the genetic variance among maize genotypes is provided by the study of molecular characterisation using SSR markers. It facilitates the formation of heterotic groupings, the identification of genetically different inbred lines, and the removal of duplicates. Long-term conservation efforts are supported, germplasm utilisation is enhanced and effective parental selection is encouraged. Future genomic and marker-assisted breeding initiatives may be built upon the molecular profiles produced.

11. Objectives

The current study on "Genetic analysis for grain yield and its contributing traits in single *v/s* three-way cross in maize (*Zea mays* L.)" will be conducted with the following objectives:

1. To estimate the heterosis for grain yield and its components in single *v/s* three-way cross maize hybrids
2. To estimate the general combining ability (gca) effects and specific combining ability (sca) effects of parents and crosses, respectively for grain yield and its component traits
3. To study the nature and magnitude of gene action governing grain yield and its component traits
4. To identify promising maize hybrids by comparing the performance of single *v/s* three-way cross
5. To characterize maize genotypes using SSR markers

12. Review of Literature

The literature pertaining to the heterosis, combining ability analysis, gene action, stability and parental diversity for grain yield and its component traits in maize has been reviewed under the following subheads:

12.1 Heterosis

Hybrid vigour is the term used to describe heterosis, or a hybrid's enhanced performance above its parents. The first person to document heterosis in plants was Koelreuter (1763), who also found that vigour increases with parental diversity. The term "heterosis" as we understand it today was originally used by Shull (1914). Fonseca and Patterson (1968) and Mather and Jinks (1971) coined a new term, "heterobeltiosis", to describe the improvement of a heterozygote in comparison to a superior parent.

Mukhlif *et al.* (2021) investigated eight genotypes were compared using a randomised complete block design (RCBD) and single crossings with half diallel cross. Heterosis Relative to Mean Parents revealed that 28 crosses in traits of days to 50% silking, 27 crosses in plant height, 20 crosses for number of ears per plants per plant, 28 in number of grains per row and grains yield per plant and 26 crosses at a 300 grain weight produced Heterosis Relative to Mean Parents in the desired significant direction in single crosses. (Zm-1, Zm-2, Zm-3, Zm-4, Zm-5, S2, S5 and S6)

Hadi *et al.* (2023) assessed performance and calculate the heterosis for grain yield (GY) and associated variables, 30 three-way cross hybrids of maize and five parental inbred lines were examined in four replications. For the qualities under study, the majority of the three-way cross hybrids outproduced their parents inbred lines. The best hybrids were found to be TW8 and TW10, with average yields of 219 gm/plant and 214 gm/plant, respectively and positive heterosis of 72% and 62%.

Sorsa *et al.* (2023) studied the degree of heterosis and assess how well three-way crossings performed in contrast to single crosses for yield and associated agronomic parameters. While TWC 14 (52%) and TWC 24 (78%) were the highest better and mid-parent heterosis, respectively, in Ambo, TWC1 (56%) and TWC30 (25%) were the highest BPH and MPH, respectively, in Melkassa, the maximum better and mid-parent heterosis was from single cross 1 (769%) in Ambo and single cross 7 (104%) in Melkassa.

Tejaswini *et al.* (2023) investigations on heterosis in maize demonstrated that during days to silking and anthesis silking interval, eighteen out of nine hybrids exhibited significantly negative heterosis over the better parent. For days to maturity, 25 hybrids showed noticeably negative standard heterosis. In terms of plant height and shelling %, ten hybrids showed considerably negative standard heterosis. Better-parent heterosis for ear girth varied from -21.18% (PFSR-73 × PFSR-127) to 17.95% (BML-10 × ML-14). For the number of kernel rows per ear, better-parent heterosis varied from -27.61% (MGC-49 × BPDT-5009) to 16.67% (ML-14 × PFSR-92). For the number of kernels per row, better-parent heterosis ranged from -39.60% (ML14 × BPDT-5009) to 50.70% (PFSR-73 × PFSR-92). For grain yield per plant, better-parent heterosis varied from -55.52% (MGC-49 × BPDT-5009) to 44.65% (PFSR-73 × ML-14).

Al-Jubouri *et al.* (2024) employed ten genotypes of maize (Gimbson, Saganto, DK 6050, Agr-183, ZM47W, CML494, IK58, ZP505, ZP670 and ZP197). In seven

traits (number of ears per plant, ears length, number of rows per ear, number of kernels per ear and plant yield), they were introduced into half diallel crosses and demonstrated heterosis as a mean parent as a percentage that superior crosses (Gimbson × ZP505), (Saganto × ZP670) and (Saganto × ZP197). In all features, including ear length, number of rows per ear, number of kernels per row and plant yield, crosses outperformed (IK58 × ZP197) in heterobeltiosis compared with a Beter parent.

12.2 Combining ability and gene action

For plant and animal breeders, the idea of general and specific combining ability as an indicator of gene activity put out by Sprague and Tatum (1942) has grown in significance. This approach divides the overall genetic variation into the effects of specific and general combining abilities. Specific combining ability (SCA) is the difference in performance of a cross combination from that predicted based on the general combining ability of the parents involved in the cross, while general combining ability (GCA) is defined as the average performance of a line in a series of crosses and is regarded as a measure of additive gene action, indicating the nicking ability of parents. It is regarded as a gauge of non-additive gene activity. In order to take advantage of transgressive segregants in breeding programmes, sca effects aid in sorting out superior crossings based on yield and other traits.

Abd El-Zaher (2021) studied seven S6 white maize inbred lines developed from S4 lines of the populations three-way cross-324 and Giza-2. These lines were crossed in a 7 × 7 half-diallel design to produce 21 F_1 hybrids, which were evaluated along with checks SC-128 and SC-129 in 2021. Significant variation was observed among genotypes, parents, and crosses for all traits, including both general and specific combining ability. The ratio of GCA to SCA variance was below unity, indicating the importance of non-additive gene action. Four crosses showed high positive heterosis for grain yield. Among them, three also exhibited earliness. Parents P_6 and P_7 were identified as strong general combiners. Dominance effects indicated over-dominance for all studied traits.

Ismail *et al*. (2023) evaluated combining ability and hybrid performance in maize using seven inbred lines crossed in a half-diallel design to produce 21 hybrids. These, along with two check hybrids, were tested in a randomized complete block design across three locations. The study revealed that both additive and non-additive gene

actions influenced all traits, with GCA variance exceeding SCA variance, indicating the predominance of additive effects. The hybrid Gz.639 × Gz.074 (213) significantly outperformed the best check (SC.168) for grain yield. Inbred lines Sk-2, Gz.639, and Gz.074 (213) showed strong general combining ability. Several crosses demonstrated significant positive SCA effects for yield, including Sk-2 × Mall.5030A and Gz.639 × Sd.3118. Some hybrids also surpassed SC.3444 in performance. These promising crosses are recommended for further multi-location testing before potential commercial release.

Billah *et al.* (2025) evaluated 20 short-statured maize inbred lines sourced from CIMMYT (India and Mexico) through Bangladesh Agricultural Research Institute. Based on diversity and performance, seven lines were selected and crossed in a 7 × 7 half-diallel design to produce 21 F_1 hybrids, which were evaluated at multiple locations. Results showed that GCA variance exceeded SCA variance for all traits, indicating the predominance of additive gene action. Parents P_3 (CML33) and P_4 (CML41) were identified as good general combiners. Crosses CML41 × CML31 and CML31 × CML124 exhibited high SCA effects and heterosis for grain yield over checks BHM 9 and NK40. Some crosses also showed desirable reduced plant height.

12. Molecular characterization using Simple Sequence Repeats (SSRs)

Simple Sequence Repeats (SSRs) are among the most promising types of molecular markers and are very helpful in genetic studies like linkage map construction and QTL mapping, as well as in the evaluation of genetic diversity and marker assisted selection (Sserumaga *et al.* 2014). Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Single Nucleotide Polymorphism (SNP) and Simple Sequence Repeats (SSRs) are a few of the frequently used molecular marker systems in genetic research. According to Sserumaga *et al*. (2014), "SSR markers are particularly favoured for their codominant nature, highly polymorphic, reproducibility and even distribution across the entire plant genome and which deliver very important information about genetic diversity, genetic relationships and population structure in crop germplasms". Short tandem repeating segments of two to six nucleotides make up SSRs, also known as microsatellites, in the plant genome. Their considerable polymorphism, seen in both coding and non-coding areas, contributes to their distinctive makeup. The unique characteristics of SSR markers, such as their polymorphism, make them useful for a number of applications, including

crop characterisation, genetic diversity evaluation and investigation of desirable gene connections [Kalivas *et al*. (2011), Gaballah e*t al.* (2021), Mathiang *et al*. (2022)].

Alaca *et al.* (2025) by applying 28 Simple Sequence Repeat (SSR) markers, examined the genetic diversity of 34 Turkish coloured maize landraces. The SSR markers' strong discriminating power and polymorphism informativeness demonstrated how useful they are for determining genetic variation. The investigation showed significant genetic variety across the landraces, with expected heterozygosity (He) values ranging from 0.1023 to 0.8832, Nei's gene diversity index (h) of 0.5458, Shannon's diversity index (I) of 1.0338 and Jaccard similarity index (J) values between 0.06 and 0.289. These results highlight the significance of Turkish coloured maize landraces as a genetic reservoir for breeding efforts centred on agronomic or qualitative parameters and show the substantial genetic variety seen in these landraces.

Farid *et al.* (2025) applied Simple Sequence Repeat (SSR) markers to analyse the genetic diversity of 30 inbred lines of maize (*Zea mays* L.) that were produced by convergent breeding. Significant genetic heterogeneity between the inbred lines of maize was found in the results. With an average of 8.42 alleles per marker, the study found 421 alleles, demonstrating strong polymorphism levels. With similarity values ranging from 0.57 to 0.85, the phylogenetic analysis divided the inbred lines into five groups that represented different levels of genetic variety. The results highlighted how crucial it is to use SSR markers to identify genetic variation in maize populations, especially those that result from convergent breeding, in order to improve breeding initiatives and create superior maize varieties.

Guo *et al.* (2025) yielded 230 polymorphic alleles using 40 Simple Sequence Repeat (SSR) primer pairs. The polymorphism information content (PIC) was calculated to evaluate the markers' ability to discriminate. The inbred lines were divided into four groups (25, 38, 97 and 40 lines, respectively) by phenotypic analysis, with benchmark lines dispersed between Groups I and III. With an average of 5.75 alleles per locus and a mean polymorphic information content (PIC) of 0.70, SSR analysis demonstrated a significant degree of genetic diversity. The population was further separated into four distinct clusters by molecular grouping, which represented 26.5%, 51.0%, 14.0% and 8.5% of the total. These clusters showed different distribution patterns than the phenotypic grouping. Benchmark lines' genetic divergence was verified by their distribution across different molecular groupings. For genetic discrimination, SSR-based clustering outperformed phenotypic grouping in

terms of robustness and reliability.

Awasthi *et al.* (2026) described 23 newly created genotypes of maize in this work, comprising four wild-type inbreds and 19 mutant gene-based genotypes. To examine allelic differences among top subtropical infant maize inbreds, new genic Simple Sequence Repeat (SSR) markers for sk1, ts1 and ts2 were created and validated. Fifteen of the twenty-four gene-specific markers were polymorphic, yielding 48 alleles with an average polymorphism information content (PIC) of 0.31 and a mean gene diversity of 0.36. The three most informative markers (PIC: 0.55–0.67) were sk15, ts21-2 and sk11. The sk1, ts1 and ts2 genes' allelic diversity showed that there were 13, 25 and 10 alleles, respectively. Additionally, molecular diversity and similarity were assessed using a total of 57 genomic SSR markers. With allele counts ranging from 2.00 to 5.00 and a maximum PIC value of 0.73 (bnlg1108), the percentage of polymorphic genomic SSRs was high (94.49%). The most informative genomic SSR markers were bnlg1108, umc1766, umc1230, bnlg1031 and umc2011.

Sathish *et al.* (2026) utilized 25 drought-associated SSR markers, a research was carried out to evaluate the genetic diversity among the twelve genotypes of maize from various sources and to identify possible parental lines for upcoming breeding initiatives. The majority of the SSR markers were polymorphic and useful for measuring the genetic diversity among the chosen genotypes of maize, according to the results. A total of 124 alleles were amplified by 25 SSR markers, with an average of 5 alleles per locus and a range of 4 to 7. The most alleles were created by markers bnlg 1179, umc 1542, bnlg 1866 and bnlg 2190. The range of the generated PCR products using 25 SSRs was 100 bp to 298 bp. Primer umc 1596 produced the greatest PCR fragment (298 bp), whereas primer bnlg 490 produced the shortest fragment (100 bp). With a mean of 0.75, the Polymorphism Information Content (PIC) value ranged from 0.70 to 0.84. Heterozygosity (H) averaged 0.79 and varied from 0.75 to 0.86. The dendrogram-based cluster analysis divided the 12 genotypes into four main groups, with cluster IV showing the greatest number of genotypes. These findings unequivocally demonstrated that the chosen genotypes had a significant degree of genetic diversity because they displayed a high degree of drought-linked SSR marker polymorphism.

13. Materials and Methods

The present investigation "Genetic analysis for grain yield and its contributing traits in single *v/s* three-way cross hybrids in maize (*Zea mays* L.)" will be carried at Instructional Farm, Department of Agronomy, JAU, Junagadh.

13.1 Location

Instructional Farm, College of Agriculture, JAU, Junagadh

13.2 Year and season of experiment

1. *Rabi* – 2025-26 (Development of single cross)
2. Summer – 2026-27 (Development of double and three-way cross)
3. *Rabi* – 2026-27 (Evaluation of single, double and three-way cross)

13.3 Experimental design

Randomized Block Design (RBD) will be used for the evalution of F_1 hybrids.

13.4 Treatment details

- Inbreds: 6
- Single crosses: 15
- Three-way crosses: 60
- Standard check: 1**(GAYMH-3)**

Sr. No.	Genotypes	Sr. No.	Genotypes
1.	IL-12 -17	**4.**	IL-14-53
2.	IL-12-38	**5.**	IL-14-68
3.	IL-14-35	**6.**	IL-14-64

13.5 No. of replication

Three replications will be examined for the performance of F_1 hybrids. The spacing between plant to plant is 20 cm and row to row is 60 cm in length.

13.6 Observation to be recorded

With the exception of days to 50 per cent tasseling, days to 50 per cent silking and days to maturity, which will be noted on a plot basis, observations on various quantitative characteristics will be recorded in each plot on five randomly tagged plants. The following characters will have different observations recorded in accordance with regular practice:

13.6.1 Days to 50 per cent tasseling

The number of days between the date of planting and the start of tassel in 50 per cent of the plants in each plot will be noted.

13.6.2 Days to 50 per cent silking

It will be noted how many days it took for 50 per cent of the plants in each plot to start producing silk from the date of seeding.

13.6.3 Days to maturity

From the date of sowing until the husk dries in 80 per cent of the plants in each plot, the number of days will be noted.

13.6.4 Plant height (cm)

At the time of maturity, the height of each of the five randomly chosen plants will be measured in cm from ground level to the base of the tassel. We'll calculate the average height of each plant.

13.6.5 Cob height (cm)

The cob height of each tagged and randomly selected five plants will be measured in centimetre from the ground level to the base of the upper most cob at the time of maturity. The mean cob height per plant will be worked out.

13.6.6 Cob length (cm)

The cob from the five randomly selected and tagged plants will be taken for measuring the length of cob.

13.6.7 Cob girth (cm)

The cob will be used to measure its average girth in cm as well as its length. The length of the thread, which will be measured in centimetres as cob girth, will be wrapped around the central part of the cob. Five cob girths will be measured, and the mean cob girth will be calculated.

13.6.8 Cob weight (g)

The cob from the five randomly selected and tagged plants will be taken for measuring the weight of cob. Weight of five cob will be measured in gram and average will be calculated.

13.6.9 Number of rows per cob

After dehusking, the number of rows per cob will be counted using the cob from the five randomly chosen and tagged plants. We'll calculate the average numbers of grain rows each cob.

13.6.10 Number of grains per row

The number of grains in each row will be counted using the cob from the five randomly chosen and labelled plants. We'll calculate the average grain values for each row.

13.6.11 Shelling percentage

The percentage cob will be calculated by dividing the weight of the seed grains by the total weight of the cobs of five randomly chosen plants.

$$\textbf{Shelling percentage} = \frac{\textbf{Total grain weight (g)}}{\textbf{weight of cob (g)}} \times \mathbf{100}$$

13.6.12 100-grain weight (g)

A composite sample of 100 grains from five randomly chosen plants per plot will be gathered and weighed in order to record the 100-grain weight in grams.

13.6.13 Grain yield per plant (g)

The five randomly chosen and tagged plants' cobs will be shelled, and the cob's seed will be weighed in grams. Following sun drying, the average grain yield per plant will be calculated.

14. Statistical Analysis

The following methods will be used to statistically analyse the mean values of the parents and F_1 hybrids for each character:

14.1 Analysis of variance for experimental design

According to Panse and Sukhatme (1995), the Randomised Block Design will be used independently for each character in the analysis of variance for the experimental design.

14.2 Estimation of heterosis

It is more plausible to estimate heterosis over superior parents and over routine checks. Therefore, heterosis will be calculated over better parent (BP) and standard check (SC) in the current study; they are referred to as heterobeltiosis and standard heterosis, respectively.

14.2.1 Heterobeltiosis

Fonseca and Patterson (1968) defined heterobeltiosis as the deviation of F_1 above the superior parent. This variance may be expressed as a percentage using the following method:

$$\textbf{Heterobeltiosis}\ (\%) = \frac{\bar{F}_1 - \overline{BP}}{\overline{BP}} \times \mathbf{100}$$

Where,

$\bar{F}_1$ = Mean performance of F_1

$\overline{BP}$ = Mean value of better parent of respective cross combination

14.2.2 Standard heterosis

It will be computed as follows and represents F_{1s} advantage over the common commercial hybrid (GAYMH-3).

$$\textbf{Standard heterosis}\ (\%) = \frac{\bar{F}_1 - \overline{SC}}{\overline{SC}} \times 100$$

Where,

$\bar{F}_1$ = Mean performance of F_1

$\overline{SC}$ = Mean performance of the standard check (GAYMH-3)

14.3 Analysis of variance for combining ability and gene action

Griffing (1956) suggested that the combining ability analysis be carried out using the half-diallel mating design.

14.4 Components of genetic variance

The components of genetic variance and other genetic ratios will be worked out using Hayman's (1954) numerical technique.

14.5 Molecular characterization using SSR markers

DNA will be extracted and purified using the Cetyl Trimethyl Ammonium Bromide (CTAB) technique, modified if necessary, as outlined by Doyle and Doyle (1990). PCR amplification of molecular markers will be performed using high-quality DNA. PCR amplification and gel electrophoresis will be carried out by using SSR (Simple Sequence Repeat) markers. The appropriate software will be used to score the PCR-amplified DNA bands and perform marker analysis.

Each molecular marker observation will be documented separately and appropriate software will be used to generate summary statistics of the molecular marker data. The proper software will be used to create the dendrogram.

14.5.1 DNA isolation

The Cetyl Trimethyl Ammonium Bromide (CTAB) technique of DNA extraction described by Doyle and Doyle (1990) will be used to extract DNA samples from genotypes. PCR amplification of molecular markers will be performed using high-quality DNA.

14.5.2 PCR amplification

The primers will be taken from the literature that is currently accessible. Ten micromoles of primer and 100 ng/ul of DNA template will be added to a 10 ul reaction for PCR amplification.

14.5.3 Gel electrophoresis

The PCR-amplified products will be resolved on a 3.0% agarose gel in 1X TBE buffer and the gel documentation system will be used to visualise them under a UV lamp.

14.5.4 Scoring of data

The co-dominant character of the SSR marker will determine how the PCR generated DNA bands are assessed.

14.5.5 Marker analysis

Appropriate molecular data analysis software will be used to the scored bands or alleles.

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